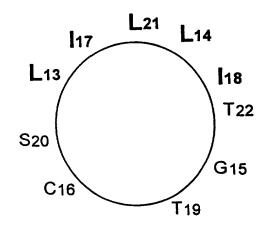
## ... T R G L<sub>13</sub> L<sub>14</sub> G C l<sub>17</sub> l<sub>18</sub> T S L<sub>21</sub> T ...



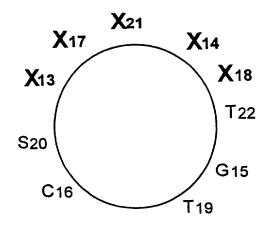
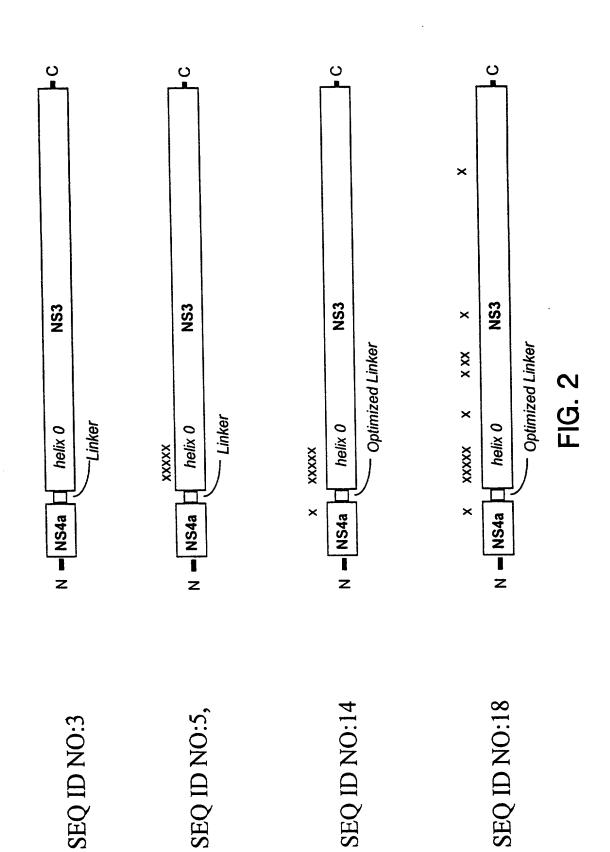
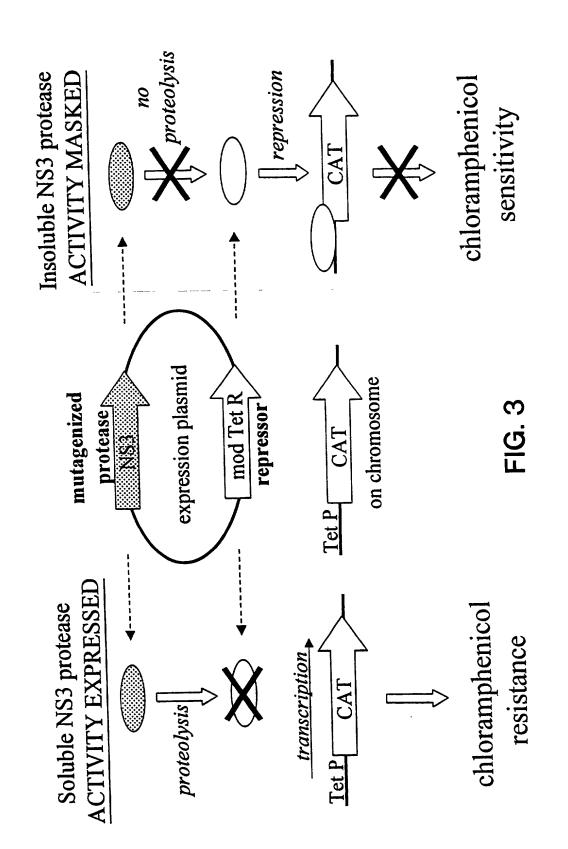
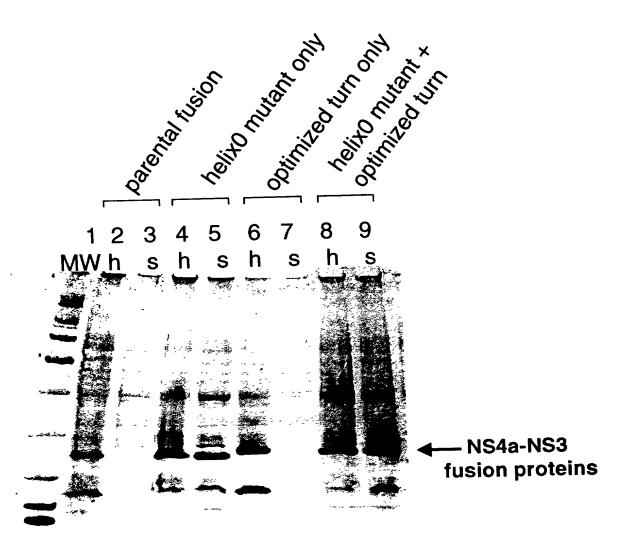


FIG. 1







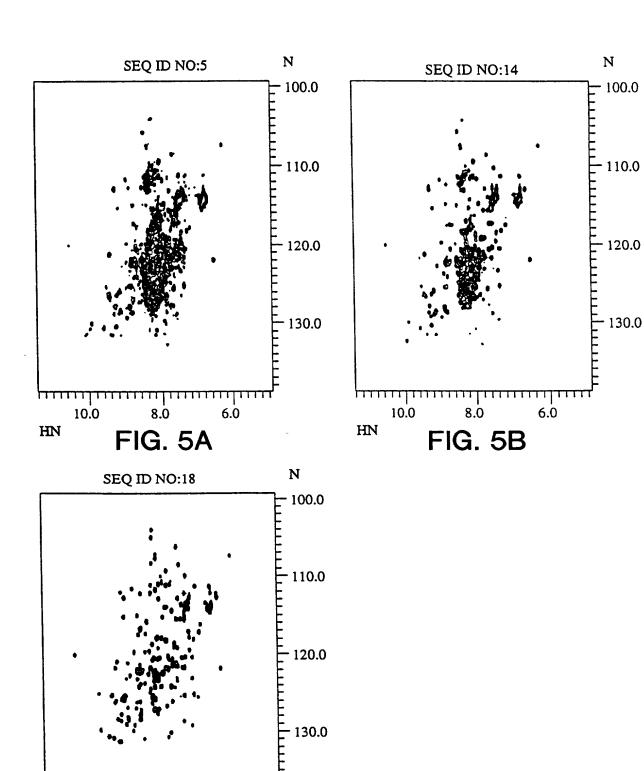
h = homogenate; s = supernatant FIG. 4

<del>ן היה היה היה היה היה ל</del> 3.0 0.0 מו

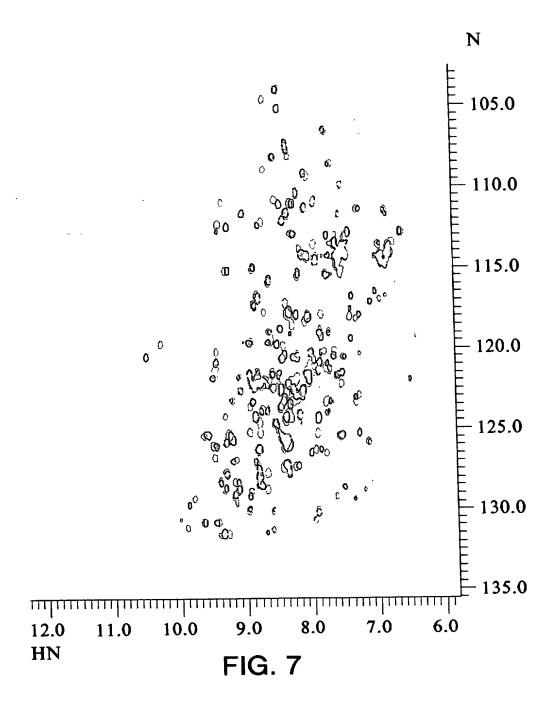
HN

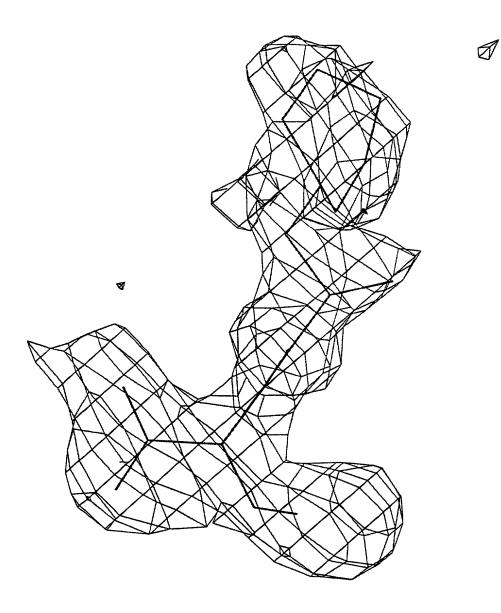
8.6 FIG. 5C

6.0



1 2 3 4 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 1 1 2 3 4 4 1 2 3 4 4 1 1 2 2 3 4 4 1 0 0 0 0 0 0 0 2 TINVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC YTNVDKDLVGWQAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLC	FIG. 6
5 0 0  MKKRGSVVIVGRIVL-NG-AYAQQTRGLLGCIITSLTGRDKNQV MKKRGSVVIVGRIVL-NG-AYAQQTRGELGCIITSLTGRDKNQV MKKRGSVVIVGRIVL-NG-AYAQQTRGEEGCQETSQTGRDKNQV MKKRGSVVIVGRINLSGDTAYAQQTRGEEGCQETSQTGRDKNQV MKKRGSVVIVGRINLSGDTAYAQQTRGEEGCQETSQTGRDKNQV MKKRGSVVIVGRINLSGDTAYAQQTRGEGCQETSQTGRDKNQV MKKRGSVVIVGRINLSGDTAYAQQTRGEGCCQKTSHTGRDKNQV MKKRGSVVIVGRINLSGDTAYAQQTRGEQCCQKTSHTGRDKNQV	T 1 1 1 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 1 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Seq ID NO:1 Seq ID NO:3 Seq ID NO:12 Seq ID NO:14 Seq ID NO:16 Seq ID NO:20 Seq ID NO:22 Seq ID NO:22	Seq ID NO:1 Seq ID NO:3 Seq ID NO:12 Seq ID NO:14 Seq ID NO:16 Seq ID NO:20 Seq ID NO:22 Seq ID NO:22	Seq ID NO:1 Seq ID NO:3 Seq ID NO:12 Seq ID NO:14 Seq ID NO:16 Seq ID NO:20 Seq ID NO:22 Seq ID NO:22





1.00 A

MAPI TAY AQQ TRGL L G C 1 ATGGCTCCGAT CACCGCTTA CGCTCAGCAG ACCCGTGGTC TGCTGGGTTG CATCATCACC TACCGAGGCT AGTGGCGAAT GCGAGTCGTC TGGGCACCAG ACGACCCAAC GTAGTAGTGG L T G RDK N O V E G E V O I V ST A 61 TCCCTGACCG GTCGTGACAA AAACCAGGTT GAAGGTGAAG TTCAGATCGT TTCCACCGCT AGGGACTGGC CAGCACTGTT TTTGGTCCAA CTTCCACTTC AAGTCTAGCA AAGGTGGCGA AQTF LAT С I N G V C W T V Y 121 GCTCAGACCT TCCTGGCTAC CTGCATCAAC GGTGTTTGCT GGACCGTTTA CCACGGTGCT CGAGTCTGGA AGGACCGATG GACGTAGTTG CCACAAACGA CCTGGCAAAT GGTGCCACGA IAS PKG PVIO R T MYT 181 GGTACCCGTA CCATCGCTTC CCCGAAAGGT CCGGTTATCC AGATGTACAC CAACGTTGAC CCATGGGCAT GGTAGCGAAG GGGCTTTCCA GGCCAATAGG TCTACATGTG GTTGCAACTG G W P APQ G S R S L T P T C K D L V 241 AAAGACCTGG TTGGTTGGCC GGCTCCGCAG GGTTCCCGTT CCCTGACCCC GTGCACCTGC TTTCTGGACC AACCAACCGG CCGAGGCGTC CCAAGGGCAA GGGACTGGGG CACGTGGACG V T R I P V S S D L Y L H A D V RRR 301 GGTTCCTCCG ACCTGTACCT GGTTACCCGT CACGCTGACG TTATCCCGGT TCGTCGTCGT CCAAGGAGGC TGGACATGGA CCAATGGGCA GTGCGACTGC AATAGGGCCA AGCAGCAGCA L S P RPI Y L K G D S R G S L 361 GGTGACTCCC GTGGTTCCCT GCTGTCCCCG CGTCCGATCT CCTACCTGAA AGGTTCCTCC CCACTGAGGG CACCAAGGGA CGACAGGGGC GCAGGCTAGA GGATGGACTT TCCAAGGAGG L C P AGH AVGI FRA A V C 421 GGTGGTCCGC TGCTGTGCCC GGCTGGTCAC GCTGTTGGTA TCTTCCGTGC TGCTGTTTGC CCACCAGGCG ACGACACGGG CCGACCAGTG CGACAACCAT AGAAGGCACG ACGACAAACG I P V E SLE T М V D F R G V AKA 481 ACCCGTGGTG TTGCTAAAGC TGTTGACTTC ATCCCGGTTG AATCCCTGGA AACCACCATG

R S \*
541 CGTTCCTGA
GCAAGGACT

FIG. 9

TGGGCACCAC AACGATTTCG ACAACTGAAG TAGGGCCAAC TTAGGGACCT TTGGTGGTAC

DFIP

V E S

- V I V MKKK G S V GRIV L N G 1 ATGAAAAAA AAGGTTCCGT TGTTATCGTC GGCCGTATAG TACTGAACGG TGCTTACGCT TACTITITIT TICCAAGGCA ACAATAGCAG CCGGCATATC ATGACTIGCC ACGAATGCGA OOTR G L L G C I I T S L TGR D K N CAGCAGACTC GAGGTCTGCT GGGTTGCATC ATCACCTCCC TGACCGGTCG TGACAAAAAC GTCGTCTGAG CTCCAGACGA CCCAACGTAG TAGTGGAGGG ACTGGCCAGC ACTGTTTTTG I V S T F L QVEG E V O TAAO 121 CAGGTTGAAG GTGAAGTTCA GATCGTTTCC ACCGCTGCTC AGACCTTCCT GGCTACCTGC GTCCAACTTC CACTTCAAGT CTAGCAAAGG TGGCGACGAG TCTGGAAGGA CCGATGGACG NGVCWT VYH GAGT RT 181 ATCAACGGTG TTTGCTGGAC CGTTTACCAC GGTGCTGGTA CCCGTACCAT CGCTTCCCCG TAGTTGCCAC AAACGACCTG GCAAATGGTG CCACGACCAT GGGCATGGTA GCGAAGGGGC L V G T N V D K D WPA KGPV I O M Y 241 AAAGGTCCGG TTATCCAGAT GTACACCAAC GTTGACAAAG ACCTGGTTGG TTGGCCGGCT TTTCCAGGCC AATAGGTCTA CATGTGGTTG CAACTGTTTC TGGACCAACC AACCGGCCGA Y L V R S L P C T C G S S D L POGS 301 CCGCAGGGTT CCCGTTCCCT GACCCCGTGC ACCTGCGGTT CCTCCGACCT GTACCTGGTT GGCGTCCCAA GGGCAAGGGA CTGGGGCACG TGGACGCCAA GGAGGCTGGA CATGGACCAA D V I P V R R R G D S R G TRHA 361 ACCCGTCACG CTGACGTTAT CCCGGTTCGT CGTCGTGGTG ACTCCCGTGG TTCCCTGCTG TGGGCAGTGC GACTGCAATA GGGCCAAGCA GCAGCACCAC TGAGGGCACC AAGGGACGAC SPRP I S Y LKG S S G G PLL 421 TCCCCGCGTC CGATCTCCTA CCTGAAAGGT TCCTCCGGTG GTCCGCTGCT GTGCCCGGCT AGGGGCGCAG GCTAGAGGAT GGACTTTCCA AGGAGGCCAC CAGGCGACGA CACGGGCCGA ĸ V CTR G V A GHAV G I F RAA 481 GGTCACGCTG TTGGTATCTT CCGTGCTGCT GTTTGCACCC GTGGTGTTGC TAAAGCTGTT CCAGTGCGAC AACCATAGAA GGCACGACGA CAAACGTGGG CACCACAACG ATTTCGACAA
  - FIG. 10

TMRS

P \*

LET

541 GACTTCATCC CGGTTGAATC CCTGGAAACC ACCATGCGTT CCCCGTGA CTGAAGTAGG GCCAACTTAG GGACCTTTGG TGGTACGCAA GGGGCACT

<u> </u>						L <sub>13</sub> L <sub>14</sub>			I <sub>17</sub> I <sub>18</sub>			L <sub>21</sub>				
Wild-type	(5) Q	Q	T	R	G	L	L	G	С	I	I	Т	s	L	Т	
Helix0-1	(6) .			•		E	E		•	Q	Ε		•	Q	•	
Helix0-3	(7) .		•			E	E			Q	Q	•		Ε	•	
Helix0-4	(8).	•	•	•	•	N	Q		•	E	K	•	•	E	•	
Helix0-7	(9) .				•	E	Q		•	Q	K		•	Н		
Helix0-8	(10).	•	•	•	•	E	Q	•	٠	D	E	•	•	E	•	
Helix0-10	(11).					E	E			E	Q	•		E	•	

FIG. 11

DFIP

V E S

M K K K G S V V I V G R I V L N G AYA 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATAG TACTGAACGG TGCTTACGCT TACTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATATC ATGACTTGCC ACGAATGCGA GEE G C Q QQTR E T S Q T G R DKN 61 CAGCAGACTC GAGGTGAGGA GGGTTGCCAA GAAACCTCCC AGACCGGTCG TGACAAAAAC GTCGTCTGAG CTCCACTCCT CCCAACGGTT CTTTGGAGGG TCTGGCCAGC ACTGTTTTTG E V Q T F L OVEG I V S TAAQ 121 CAGGTTGAAG GTGAAGTTCA GATCGTTTCC ACCGCTGCTC AGACCTTCCT GGCTACCTGC GTCCAACTTC CACTTCAAGT CTAGCAAAGG TGGCGACGAG TCTGGAAGGA CCGATGGACG INGVCWT V Y H GAGT RTI 181 ATCAACGGTG TTTGCTGGAC CGTTTACCAC GGTGCTGGTA CCCGTACCAT CGCTTCCCCG TAGTTGCCAC AAACGACCTG GCAAATGGTG CCACGACCAT GGGCATGGTA GCGAAGGGGC V D K D KGPV I O M Y T N L V G 241 AAAGGTCCGG TTATCCAGAT GTACACCAAC GTTGACAAAG ACCTGGTTGG TTGGCCGGCT TTTCCAGGCC AATAGGTCTA CATGTGGTTG CAACTGTTTC TGGACCAACC AACCGGCCGA P Q G S R S L T P C TCGS S D L 301 CCGCAGGGTT CCCGTTCCCT GACCCCGTGC ACCTGCGGTT CCTCCGACCT GTACCTGGTT GGCGTCCCAA GGGCAAGGGA CTGGGGCACG TGGACGCCAA GGAGGCTGGA CATGGACCAA TRHA DVI P V R RRGD SRG 361 ACCCGTCACG CTGACGTTAT CCCGGTTCGT CGTCGTGGTG ACTCCCGTGG TTCCCTGCTG TGGGCAGTGC GACTGCAATA GGGCCAAGCA GCAGCACCAC TGAGGGCACC AAGGGACGAC SPRP S S G G I S Y LKG PLL 421 TCCCCGCGTC CGATCTCCTA CCTGAAAGGT TCCTCCGGTG GTCCGCTGCT GTGCCCGGCT AGGGGCGCAG GCTAGAGGAT GGACTTTCCA AGGAGGCCAC CAGGCGACGA CACGGGCCGA V C T R GIF R A A G V A K A V GHAV 481 GGTCACGCTG TTGGTATCTT CCGTGCTGCT GTTTGCACCC GTGGTGTTGC TAAAGCTGTT CCAGTGCGAC AACCATAGAA GGCACGACGA CAAACGTGGG CACCACAACG ATTTCGACAA

FIG. 12

TMRS

р

LET

541 GACTTCATCC CGGTTGAATC CCTGGAAACC ACCATGCGTT CCCCGTGA CTGAAGTAGG GCCAACTTAG GGACCTTTGG TGGTACGCAA GGGGCACT

- M K K K G S V V I V G R I N L S G D T A

  1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
  TACTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA
- Y A Q Q T R G E E G C Q E T S Q T G R D 61 TACGCTCAGC AGACTCGAGG TGAGGAGGGT TGCCAAGAAA CCTCCCAGAC CGGTCGTGAC ATGCGAGTCG TCTGAGCTCC ACTCCTCCCA ACGGTTCTTT GGAGGGTCTG GCCAGCACTG
- K N Q V E G E V Q I V S T A A Q T F L A

  121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTGCTCAGAC CTTCCTGGCT
  TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GACGAGTCTG GAAGGACCGA
- T C I N G V C W T V Y H G A G T R T I A
  181 ACCTGCATCA ACGGTGTTTG CTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
  TGGACGTAGT TGCCACAAAC GACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA
- S P K G P V I Q M Y T N V D K D L V G W 241 TCCCCGAAAG GTCCGGTTAT CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG AGGGGCTTTC CAGGCCAATA GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC
- PAPQ GSRSLTPCTCCTGACC CCGTGCACCT GCGGTTCCTC CGACCTGTAC GGCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG
- L V T R H A D V I P V R R R G D S R G S
  361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC
  GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG
- L L S P R P I S Y L K G S S G G P L L C 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCCT CCGGTGGTCC GCTGCTGTGC GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG
- PAGHAVGIFRAAVCTTRGVAK 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT GCACCCGTGG TGTTGCTAAA GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA CGTGGGCACC ACAACGATTT
- A V D F I P V E S L E T T M R S P \*
  541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
  CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

AVDF

I P V

MKKK G S V VIV GRIN L S G 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT TACTITITIT TICCTAGGCA ACAATAGCAG CCGGCATAGI IGGACAGGCC ACTGIGGCGA YAOO TRG E E G CQET SOT GRD 61 TACGCTCAGC AGACTCGAGG TGAGGAGGGT TGCCAAGAAA CCTCCCAGAC CGGTCGTGAC ATGCGAGTCG TCTGAGCTCC ACTCCTCCCA ACGGTTCTTT GGAGGGTCTG GCCAGCACTG E G E KNOV V O I VSTA TOT 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTACCCAGAC CTTCCTGGCT TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA TCIN G V C WTV Y H G A GTR 181 ACCTGCATCA ACGGTGTTTG CTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT TGGACGTAGT TGCCACAAAC GACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA SPKG PVT O M Y TNVD K D L VGW 241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC SLT PCTC Q A P Q G S R G S S DLY 301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCTC CGACCTGTAC GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG H A D VIP V R R R G D S 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG LLSP R P I SYL K G S S GGP 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCCT CCGGTGGTCC GCTGCTGTGC GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG PAGH A V G T R G I F R A A V C VAK 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT GCACCCGTGG TGTTGCTAAA GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA CGTGGGCACC ACAACGATTT

FIG. 14

E T

T M

R S P

E S L

541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

L S G MKKK G S V V I V GRIN ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT TACTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA S Q T TRG E E G COET G R D A 0 0 61 TACGCTCAGC AGACTCGAGG TGAGGAGGGT TGCCAAGAAA CCTCCCAGAC CGGTCGTGAC ATGCGAGTCG TCTGAGCTCC ACTCCTCCCA ACGGTTCTTT GGAGGGTCTG GCCAGCACTG VSTA TOT K N O V E G E VOI L A 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTACCCAGAC CTTCCTGGCT TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA SIN G V L WTV Y H G A GTR ጥ ፐ 181 ACCTCCATCA ACGGTGTTCT GTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT TGGAGGTAGT TGCCACAAGA CACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA PVT PKG Q M Y TNVD K D L 241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC SLT PCTC G S S D L Y Q A P O GSR 301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCTC CGACCTGTAC GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG VIP VRRR G D S LVTR H A D 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG R P I SYL K G S S G G P LLSP 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCCT CCGGTGGTCC GCTGCTGTGC GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG A A V S T R G PAGH AVG I F R 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT CCACCCGTGG TGTTGCTAAA GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA GGTGGGCACC ACAACGATTT AVDF I P V E S L ETT R S M 541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 15

- M K K K G S V V I V G R I N L S G D T A

  1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
  TACTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA
- Y A Q Q T R G E Q G C Q K T S H T G R D
  61 TACGCTCAGC AGACTCGAGG TGAGCAGGGT TGCCAGAAGA CCTCCCACAC CGGTCGTGAC
  ATGCGAGTCG TCTGAGCTCC ACTCGTCCCA ACGGTCTTCT GGAGGGTGTG GCCAGCACTG
- K N Q V E G E V Q I V S T A T Q T F L A
  121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTACCCAGAC CTTCCTGGCT
  TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA
- T S I N G V L W T V Y H G A G T R T I A

  181 ACCTCCATCA ACGGTGTTCT GTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
  TGGAGGTAGT TGCCACAAGA CACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA
- S P K G P V T Q M Y T N V D K D L V G W
  241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG
  AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC
- Q A P Q G S R S L T P C T C G S S D L Y
  301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCTC CGACCTGTAC
  GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG
- L V T R H A D V I P V R R R G D S R G S
  361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC
  GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG
- L L S P R P I S Y L K G S S G G P L L C
  421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCCT CCGGTGGTCC GCTGCTGTGC
  GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG
- PAGHAVGIFRAAVSTRGVAK 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT CCACCCGTGG TGTTGCTAAA GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA GGTGGGCACC ACAACGATTT
- A V D F I P V E S L E T T M R S P \*
  541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
  CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

V D F

I P V

- G S V V I V MKKK GRIN L S G 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT TACTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA Y A O O TRG E O G TQKT S Н R 61 TACGCTCAGC AGACTCGAGG TGAGCAGGGT ACCCAGAAGA CCTCCCACAC CGGTCGTGAC ATGCGAGTCG TCTGAGCTCC ACTCGTCCCA TGGGTCTTCT GGAGGGTGTG GCCAGCACTG KNOV E G E V O I VSTA T OT 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTACCCAGAC CTTCCTGGCT TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA I N G V L WTV Y H G A G T R 181 ACCTCCATCA ACGGTGTTCT GTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT TGGAGGTAGT TGCCACAGA CACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA SPKG PVT Y M O TNVD K D L 241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC G S R S L Т P C T С S Y OAPO 301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCTC CGACCTGTAC GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG H A D V I P VRRR D 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG SYL K G S S G G P LLSP RPI 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCCT CCGGTGGTCC GCTGCTGTGC GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG A G H A V G Ι F R A A V S T R G Α 481 CCGGCTGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT CCACCCGTGG TGTTGCTAAA GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA GGTGGGCACC ACAACGATTT
  - FIG. 17

E T

T

M

S P

R

E S L

541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

- M K K K G S V V I V GRIN L S G DTA 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT TACTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA Y A Q Q TRG LLG С IIT S L T 61 TACGCTCAGC AGACTCGAGG TCTGCTGGGT TGCATCATCA CCTCCCTGAC CGGTCGTGAC
- ATGCGAGTCG TCTGAGCTCC AGACGACCCA ACGTAGTAGT GGAGGGACTG GCCAGCACTG
- K N Q V E G E V Q I V S T A A Q T F L A 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTGCTCAGAC CTTCCTGGCT TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GACGAGTCTG GAAGGACCGA
- T C I N G V C W T V Y H G A G T R T I A 181 ACCTGCATCA ACGGTGTTTG CTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT TGGACGTAGT TGCCACAAAC GACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA
- S P K G P V I Q M Y T N V D K D L V G W 241 TCCCCGAAAG GTCCGGTTAT CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG AGGGGCTTTC CAGGCCAATA GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC
- PAPQ GSRSLTPCTCGGSSDLY

  301 CCGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCTC CGACCTGTAC
  GGCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG
- L V T R H A D V I P V R R R G D S R G S 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG
- L L S P R P I S Y L K G S S G G P L L C 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCCT CCGGTGGTCC GCTGCTGTGC GACGACAGGG GCCCACCAGG CGACGACACG
- PAGHAVGIFRAAVCTTRGVAK 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT GCACCCGTGG TGTTGCTAAA GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA CGTGGGCACC ACAACGATTT
- A V D F I P V E S L E T T M R S P \*
  541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
  CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT